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Ramunas Stepanauskas

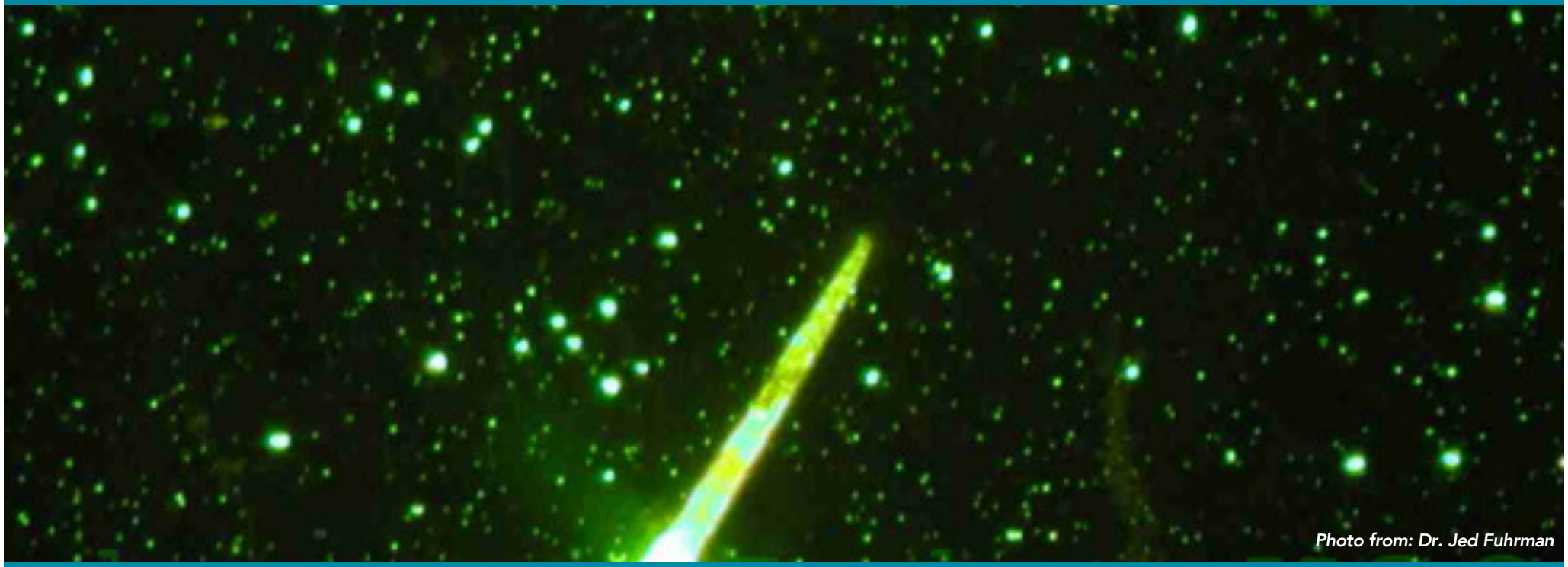


Photo from: Dr. Jed Fuhrman

Sequencing individual cells of microorganisms

Microbial planet

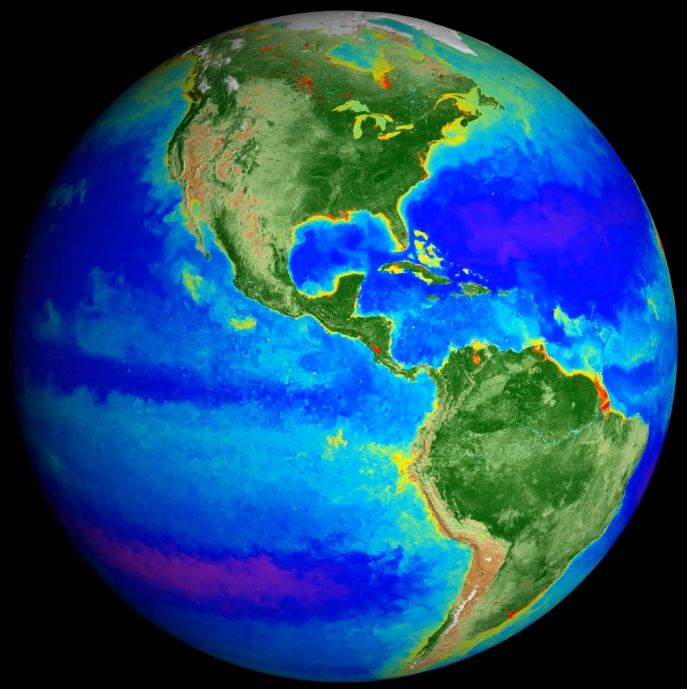


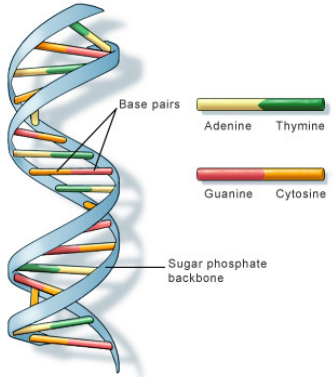
Image from: NASA

- 10^{30} cells, trillions of “species”
- Dominance of global biogeochemistry
- Enormous bioeconomy potential

Genome: organism's blueprint

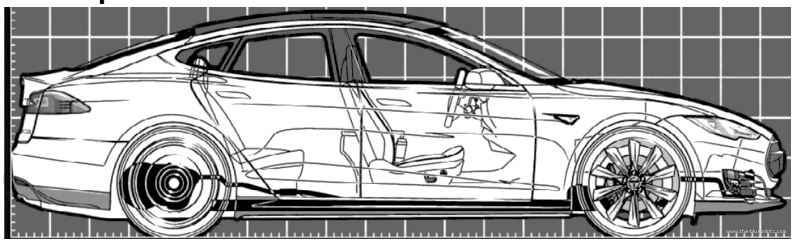
Blueprint (genome) of a microbe

From: istockphoto.com



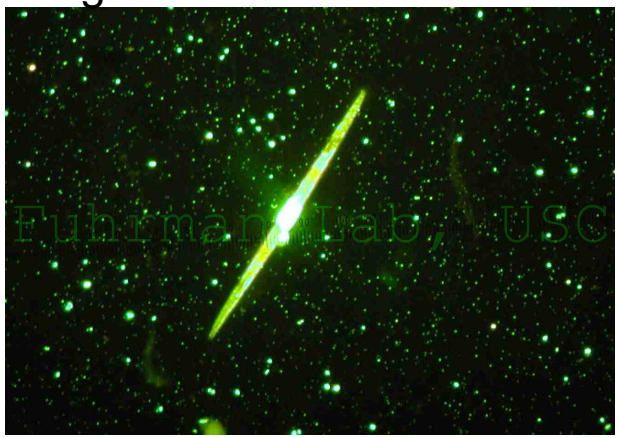
U.S. National Library of Medicine

Blueprint of a car



From: the-blueprints.com

Image of marine microbes

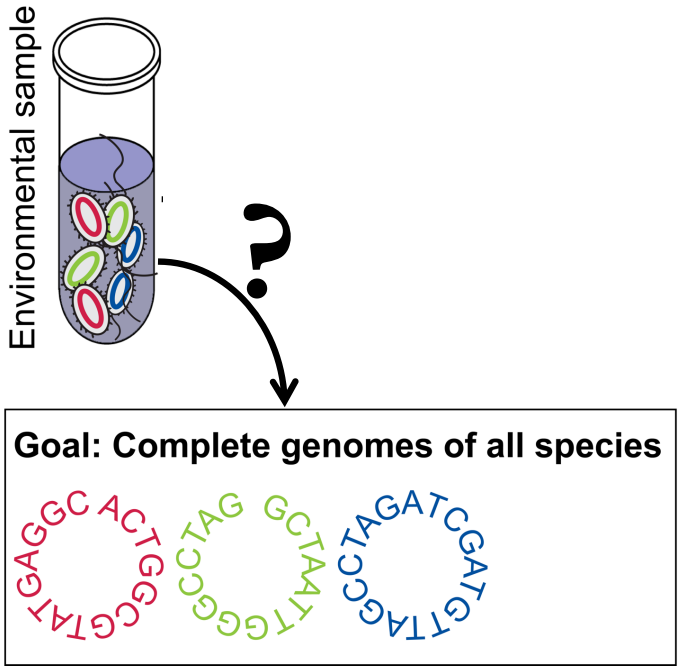


From: Jed Fuhrman

Image of a car

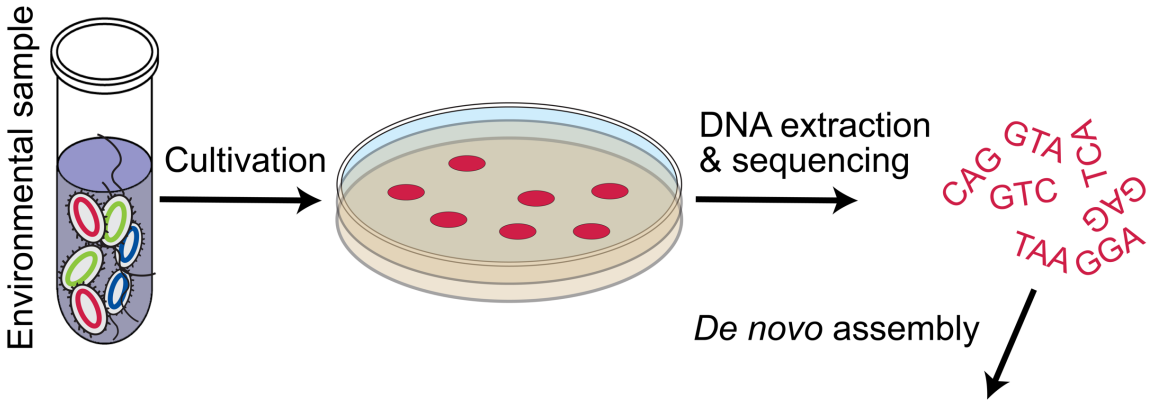
From: tautoblog.com

How do we read microbial genomes?



How do we read microbial genomes?

Approach I: Laboratory cultivation



Goal: Complete genomes of all species

Result: Genomes of <1%

How do we read microbial genomes?

Approach II: Metagenome assembly and binning

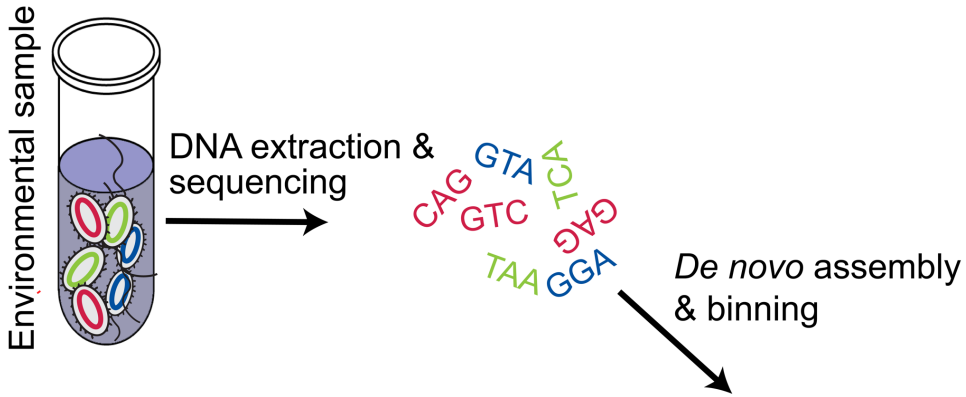


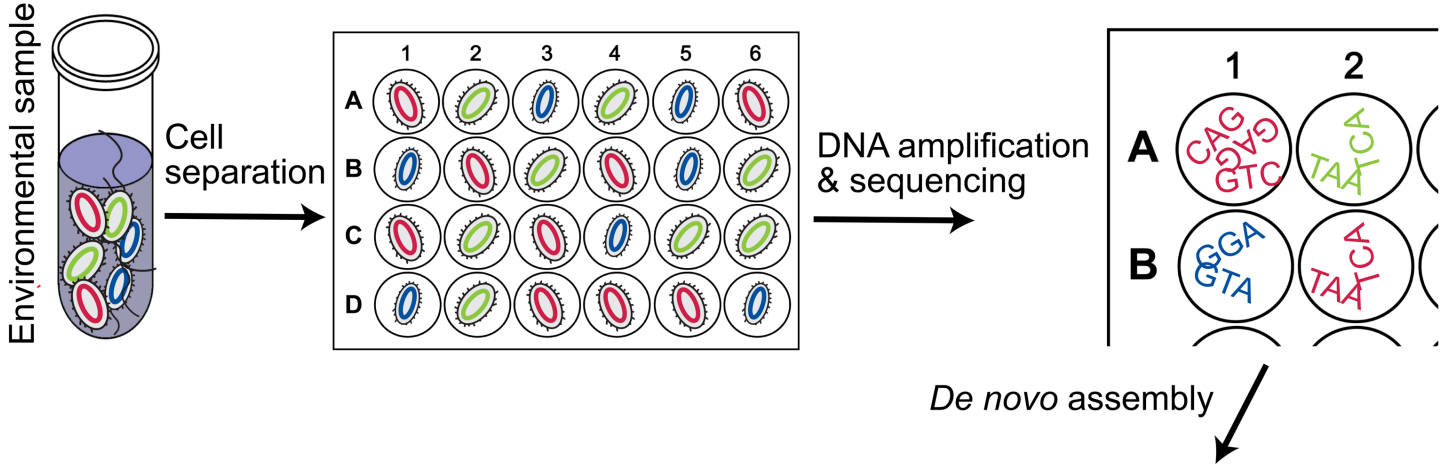
Image from: Wiktionary

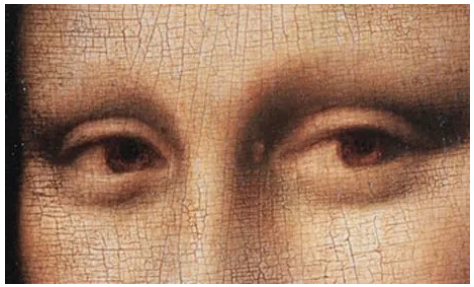
Goal: Complete genomes of all species

Result: Chimeric, incomplete genomes of some members of the community

How do we read microbial genomes?

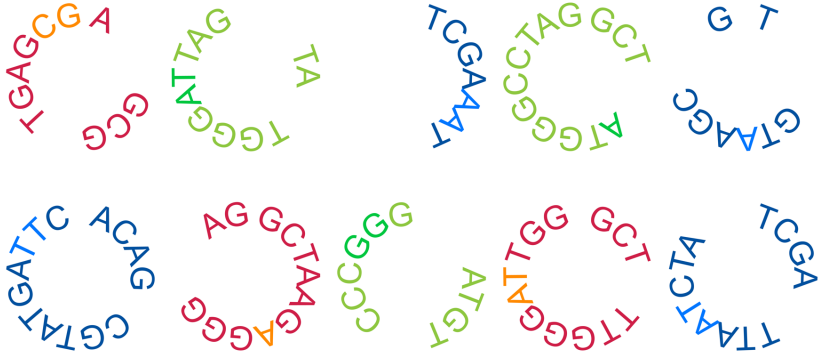
Approach III: Single cell genomics





Goal: Complete genomes of all species

Result: Randomized sample of incomplete genomes



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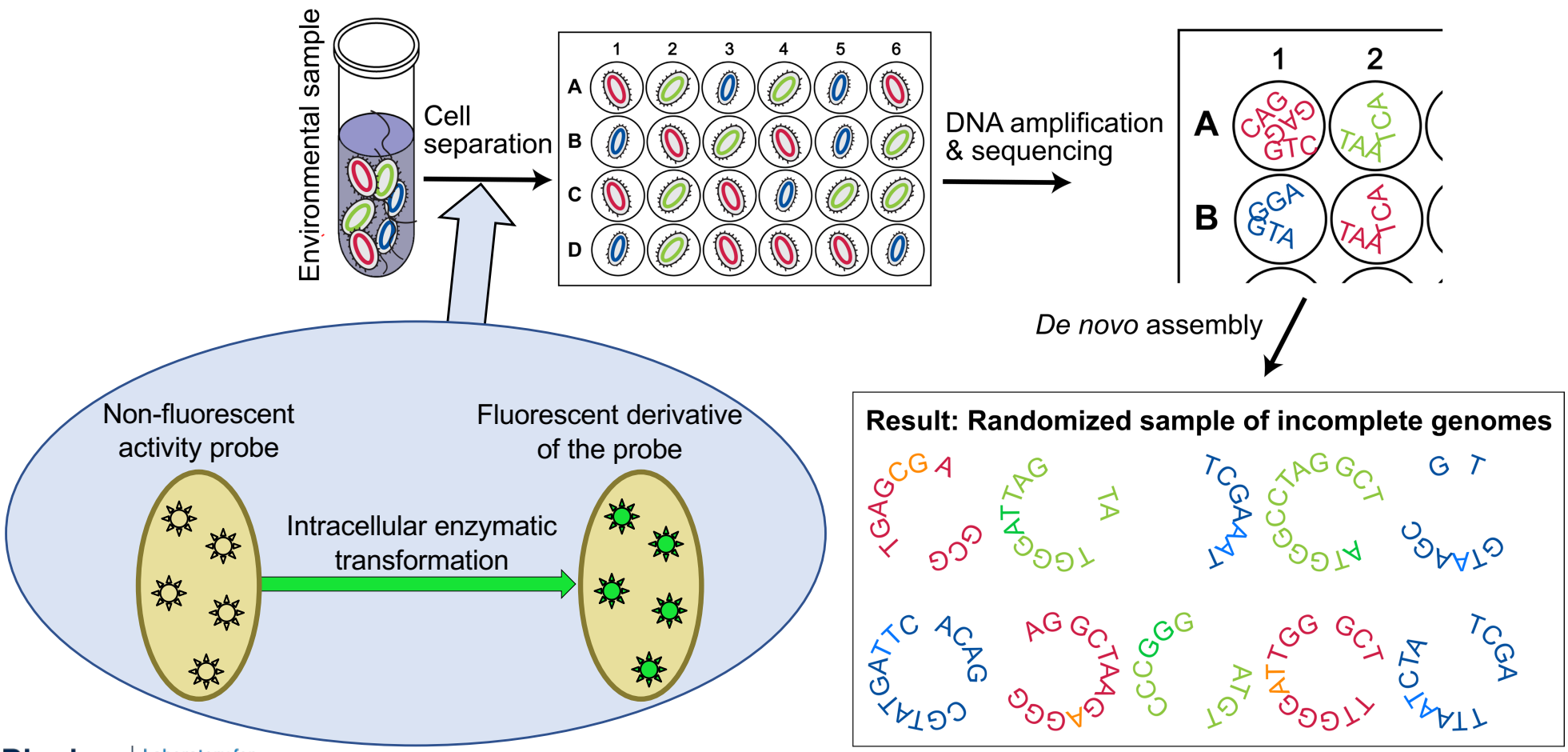
Integrated single cell genome and phenome analyses



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Beginnings of microbial single cell genomics

Cultured single cell DNA amplification

APPLIED AND ENVIRONMENTAL MICROBIOLOGY, June 2005, p. 3342–3347 Vol. 71, No. 6
0099-2240/05/$08.00+0 doi:10.1128/AEM.71.6.3342–3347.2005
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Genomic DNA Amplification from a Single Bacterium

Arumugham Raghunathan,† Harley R. Ferguson, Jr., Carole J. Bornarth,†
Wanmin Song, Mark Driscoll,‡ and Roger S. Lasken*
Molecular Staging, Inc., New Haven, Connecticut

Received 3 August 2004/Accepted 20 December 2004

ARTICLES

nature biotechnology

Sequencing genomes from single cells by polymerase cloning

Kun Zhang[1], Adam C Martiny[2], Nikos B Reppas[1], Kerrie W Barry[3], Joel Malek[4], Sallie W Chisholm[2] & George M Church[1]

Wild single cell DNA amplification

PNAS

Matching phylogeny and metabolism in the uncultured marine bacteria, one cell at a time

Ramunas Stepanauskas* and Michael E. Sieracki
Bigelow Laboratory for Ocean Sciences, P.O. Box 475, West Boothbay Harbor, ME 04575-0475

Edited by David M. Karl, University of Hawaii, Honolulu, HI, and approved April 11, 2007 (received for review January 18, 2007)

The identification of predominant microbial taxa with specific metabolic capabilities remains one the biggest challenges in environmental microbiology, because of the limits of current met-

more productive alternative for metabolic
tured microorganisms. This strategy has bee
tum, with recent implementations of single-

Wild single cell genome assembly

OPEN ACCESS Freely available online PLoS one

Assembling the Marine Metagenome, One Cell at a Time

Tanja Woyke[1], Gary Xie[2], Alex Copeland[1], José M. González[3], Cliff Han[2], Hajnalka Kiss[2], Jimmy H. Saw[2,6], Pavel Senin[2,7], Chi Yang[2,8], Sourav Chatterji[4], Jan-Fang Cheng[1], Jonathan A. Eisen[1,4], Michael E. Sieracki[5], Ramunas Stepanauskas[5]*

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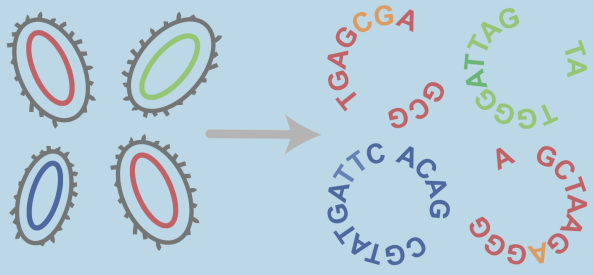
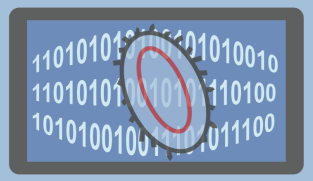
Global Ocean Reference Genomes (GORG)

28 water samples from tropical and subtropical Atlantic and Pacific oceans

Randomized genomic sequencing of 12,715 individual cells of prokaryoplankton

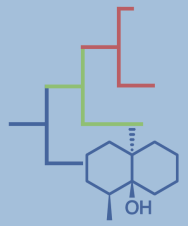


Reference genome database



Global patterns of variation

Lineage-resolved metabolism



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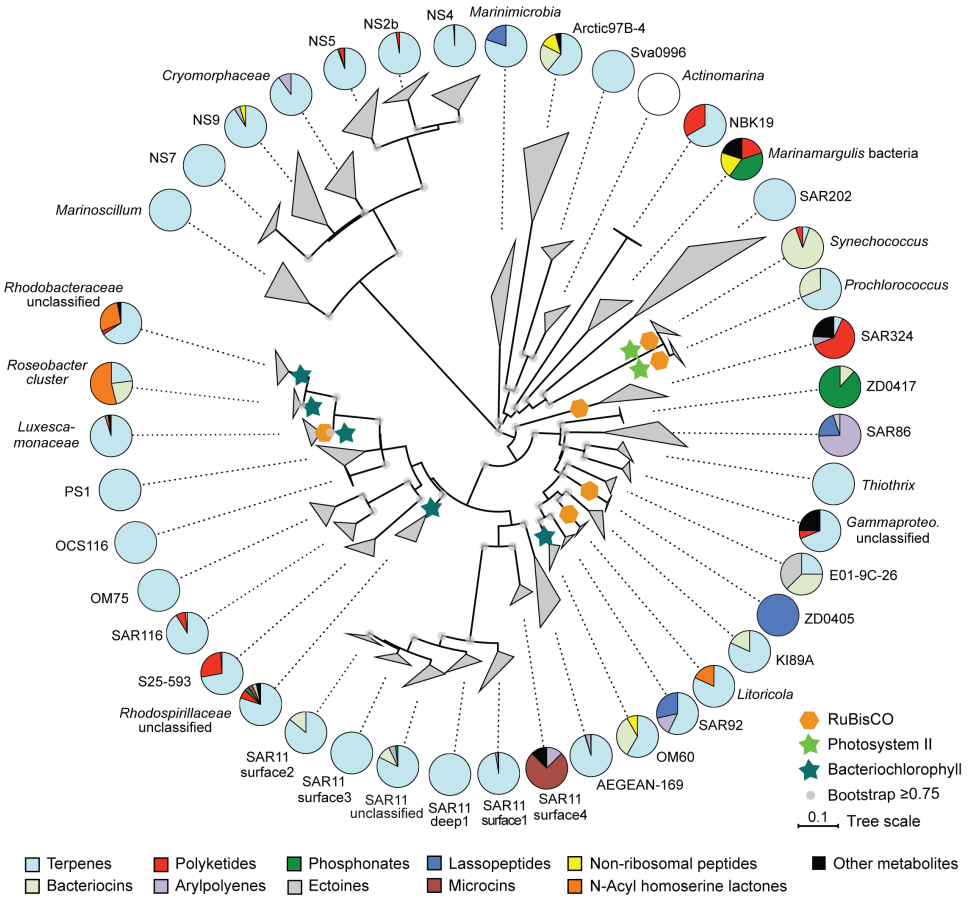
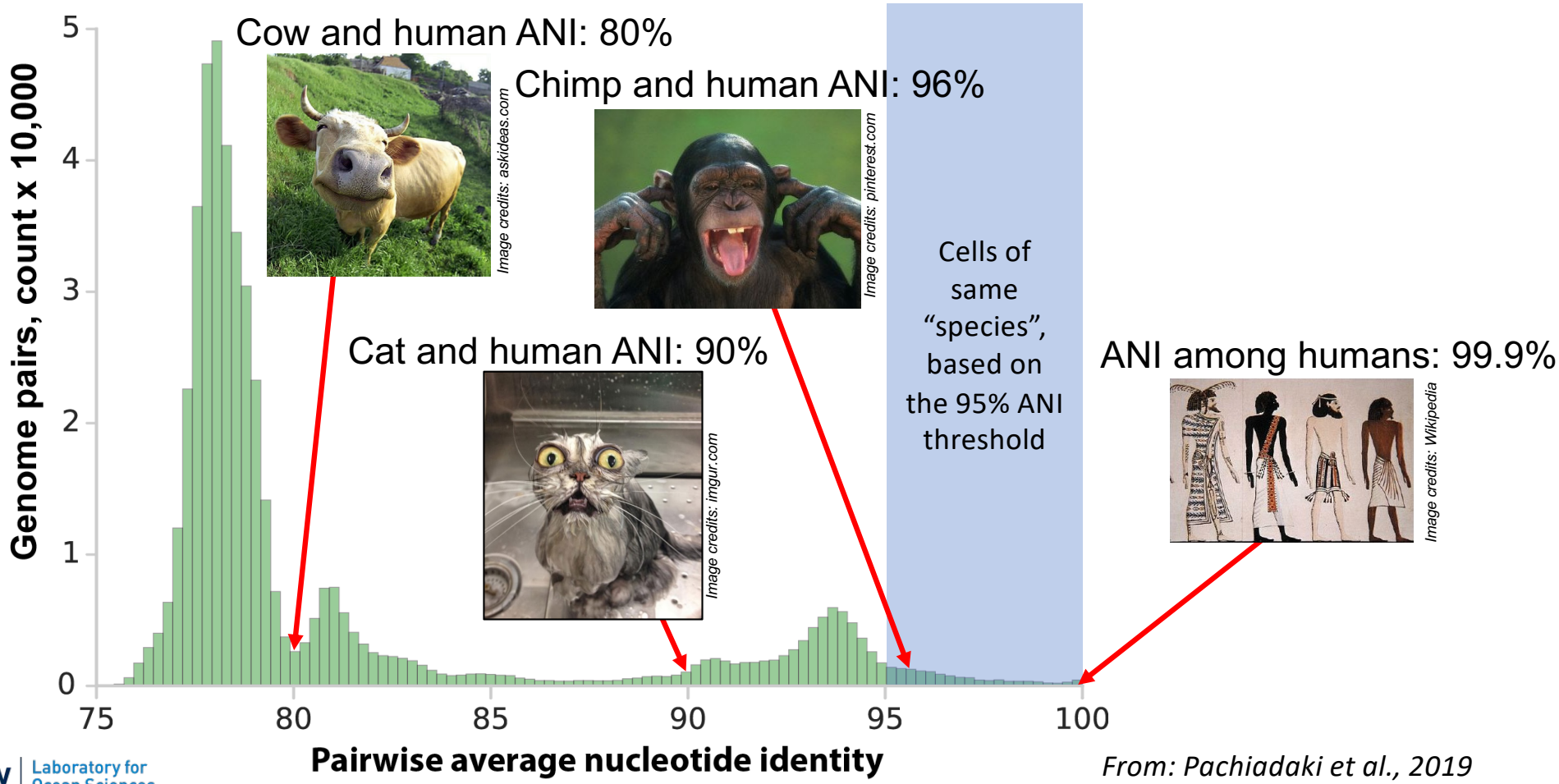


From: Pachiadaki et al., 2019, Cell

ANI of SAGs from 0.4 mL seawater



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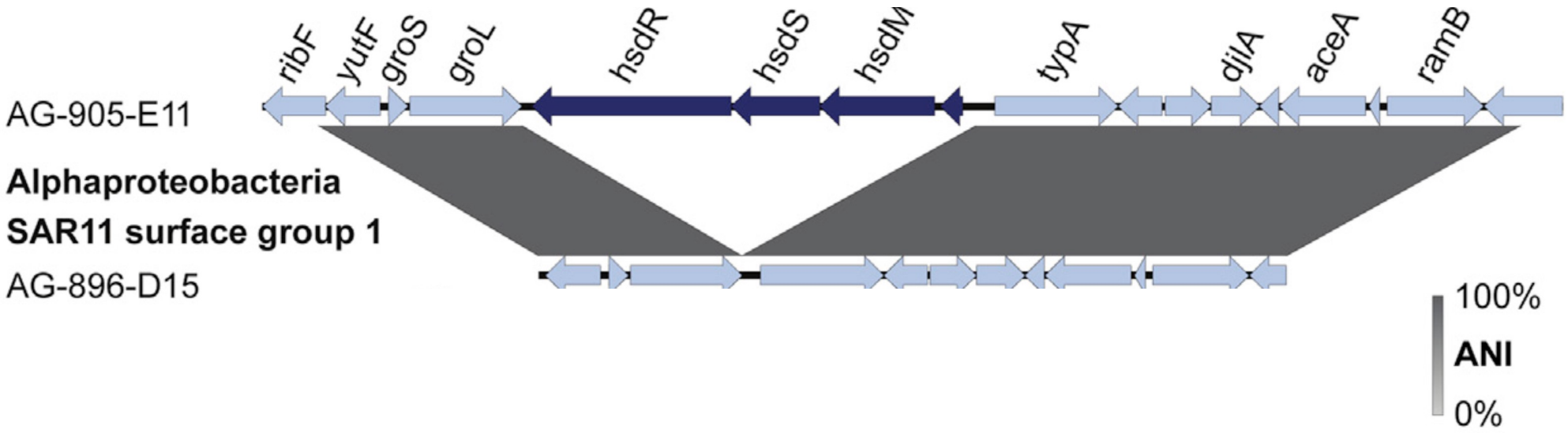
From: Pachiadaki et al., 2019

Gene content differences in genomes with >99.9% ANI



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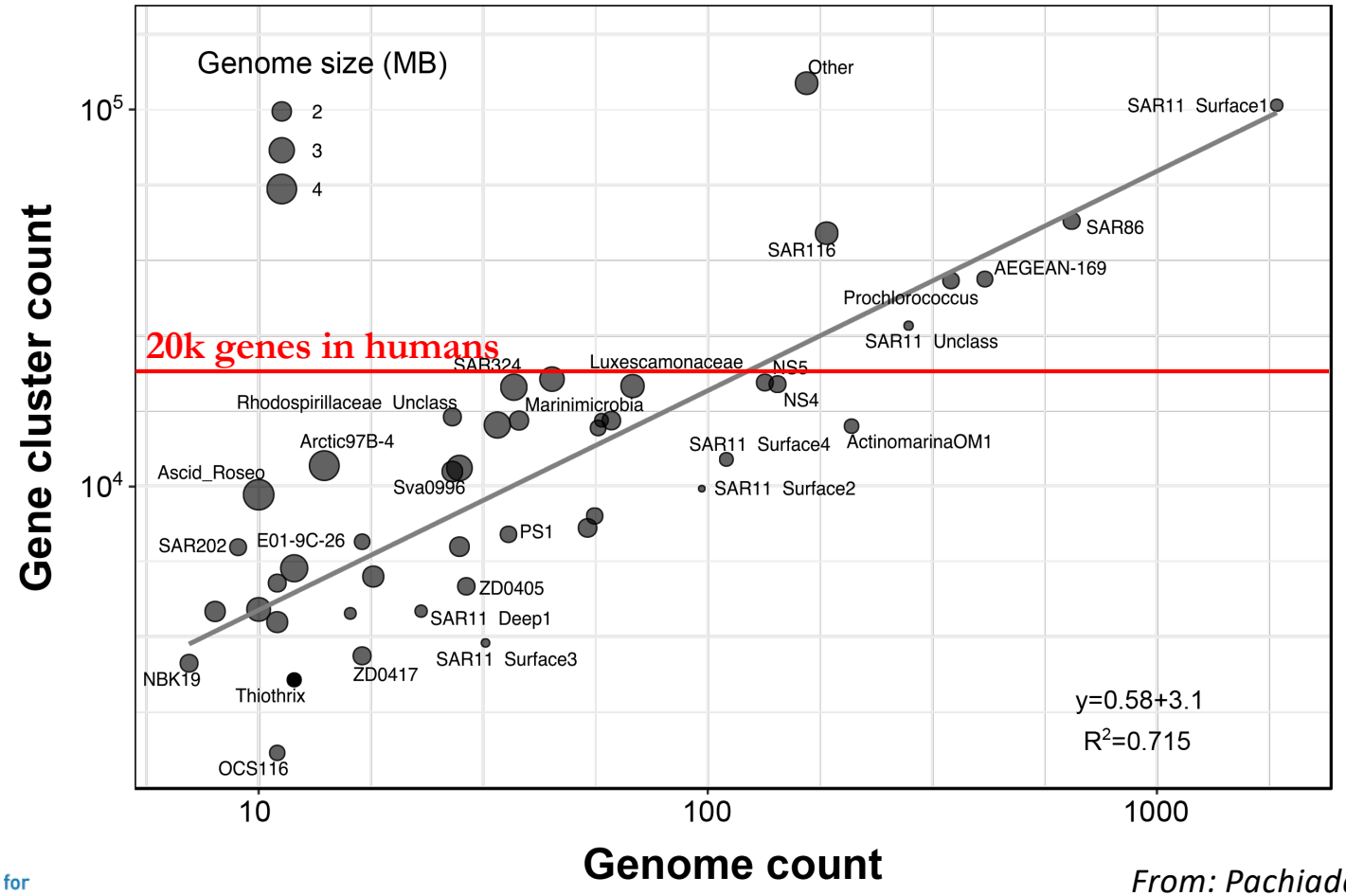
From: Pachiadaki et al., 2019, Cell

Pangenome sizes of marine microbial lineages



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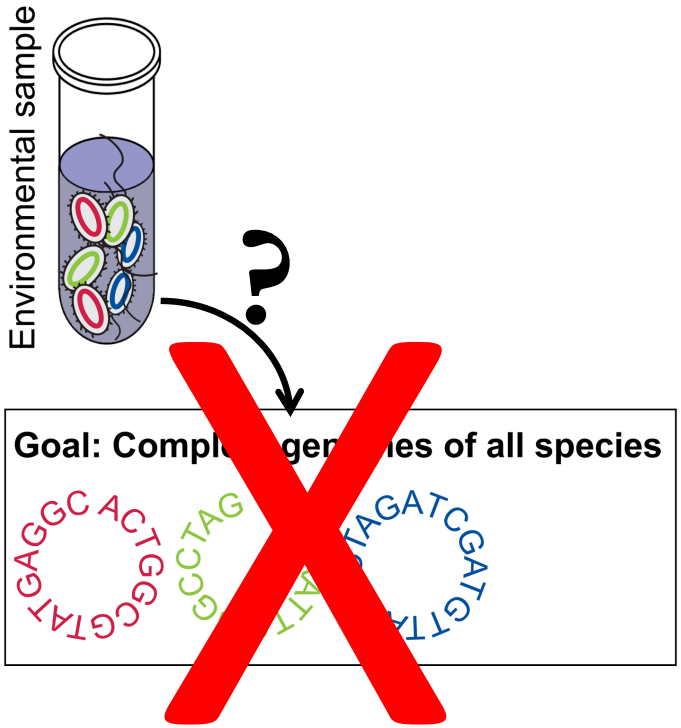
From: Pachiadaki et al., 2019, Cell

“Complete” genomes of microbial lineages do not exist



Single Cell Genomics Center (SCGC) at Bigelow Laboratory

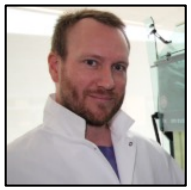
Open research and service center

First and largest facility of this type, established 2009

scgc.bigelow.com

SCGC team

Ramunas Stepanauskas, PhD
SCGC Director



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SCGC Manager

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Research Scientist

Nicole Poulton, PhD
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Corianna Mascena
Research Associate

Gregory Gavelis, PhD
Bioinformatician

Brian Thompson
Senior Research Associate

SCGC customers

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Financial support NSF SIMONS FOUNDATION mti Maine Technology Institute Investing in Innovation